FIG. 1

```
                -35                                                -10
CAACCTTGACTATTTAAATGGAACTGCCACTCCTAAAAACTAAAATATAAATACA

TTTATAAAATTTCTAAATAAACAGAAATCTGATTTTTAACTACTTACTGCTATTT
                                          SD
CATGTATTCTCGTACGAGTAATACATTTAATTAAGGAGAAAAA ATG AAA AAG      9
                                             MET Lys Lys

ATT AAC ATC ATC AAA ATA GTT TTC ATA ATT ACA GTC ATA CTG      51
Ile Asn Ile Ile Lys Ile Val Phe Ile Ile Thr Val Ile Leu

ATT TCT ACT TAT TTC ACC TAT CAT CAA AGT *GAC TCT AAG AAA     93
Ile Ser Thr Tyr Phe Thr Tyr His Gln Ser Asp Ser Lys Lys

GAC ATT TCG AAT GTT AAA AGT GAT TTA CTT TAT GCA TAC ACT      135
Asp Ile Ser Asn Val Lys Ser Asp Leu Leu Tyr Ala Tyr Thr

ATA ACT CCT TAT GAT TAT AAA GAT TGC AGG GTA AAT TTT TCA      177
Ile Thr Pro Tyr Asp Tyr Lys Asp Cys Arg Val Asn Phe Ser

ACG ACA CAC ACA TTA AAC ATT GAT ACT CAA AAA TAT AGA GGG      219
Thr Thr His Thr Leu Asn Ile Asp Thr Gln Lys Tyr Arg Gly

AAA GAC TAT TAT ATT AGT TCC GAA ATG TCT TAT GAG GCC TCT      261
Lys Asp Tyr Tyr Ile Ser Ser Glu MET Ser Tyr Glu Ala Ser

CAA AAA TTT AAA CGA GAT GAT CAT GTA GAT GTT TTT GGA TTA      303
Gln Lys Phe Lys Arg Asp Asp His Val Asp Val Phe Gly Leu

TTT TAT ATT CTT AAT TCT CAC ACC GGT GAG TAC ATC TAT GGA      345
Phe Tyr Ile Leu Asn Ser His Thr Gly Glu Tyr Ile Tyr Gly

GGA ATT ACG CCT GCT CAA AAT AAT AAA GTA AAT CAT AAA TTA      387
Gly Ile Thr Pro Ala Gln Asn Asn Lys Val Asn His Lys Leu

TTG GGA AAT CTA TTT ATT TCG GGA GAA TCT CAA CAG AAC TTA      429
Leu Gly Asn Leu Phe Ile Ser Gly Glu Ser Gln Gln Asn Leu

AAT AAC AAG ATT ATT CTA GAA AAG GAT ATC GTA ACT TTC CAG      471
Asn Asn Lys Ile Ile Leu Glu Lys Asp Ile Val Thr Phe Gln

GAA ATT GAC TTT AAA ATC AGA AAA TAC CTT ATG GAT AAT TAT      513
Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu MET Asp Asn Tyr

AAA ATT TAT GAC GCT ACT TCT CCT TAT GTA AGC GGC AGA ATC      555
Lys Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly Arg Ile

GAA ATT GGC ACA AAA GAT GGG AAA CAT GAG CAA ATA GAC TTA      597
Glu Ile Gly Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu

TTT GAC TCA CCA AAT GAA GGG ACT AGA TCA GAT ATT TTT GCA      639
Phe Asp Ser Pro Asn Glu Gly Thr Arg Ser Asp Ile Phe Ala

AAA TAT AAA GAT AAT AGA ATT ATC AAT ATG AAG AAC TTT AGT      681
Lys Tyr Lys Asp Asn Arg Ile Ile Asn MET Lys Asn Phe Ser

CAT TTC GAT ATT TAT CTT GAA AAA TAATTCATCATACACAAAAAACC
His Phe Asp Ile Tyr Leu Glu Lys TER

GCCCAGAATAATCTGAGCGGTTTTGTCTTATCTCGGAGCTTTACCTCCTAATTTA
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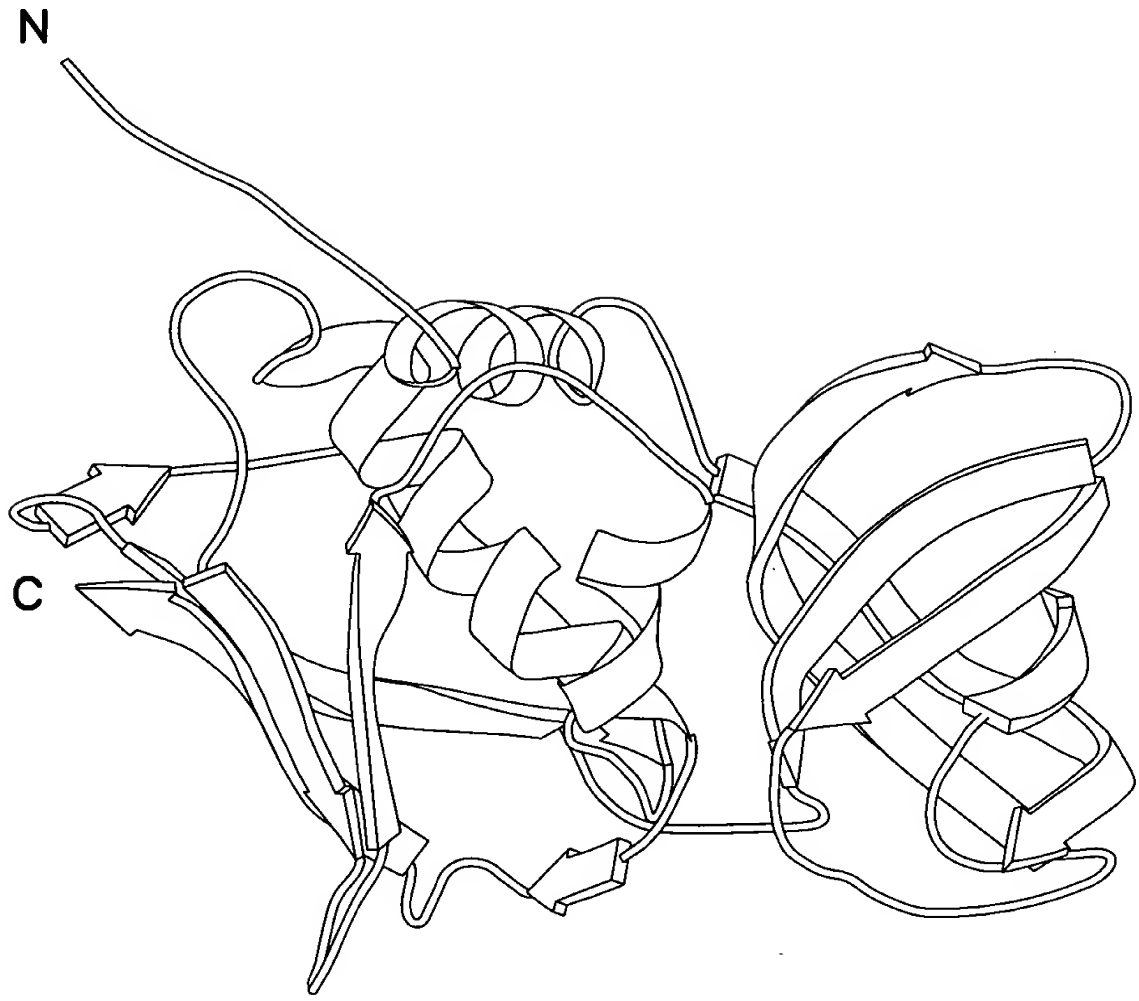
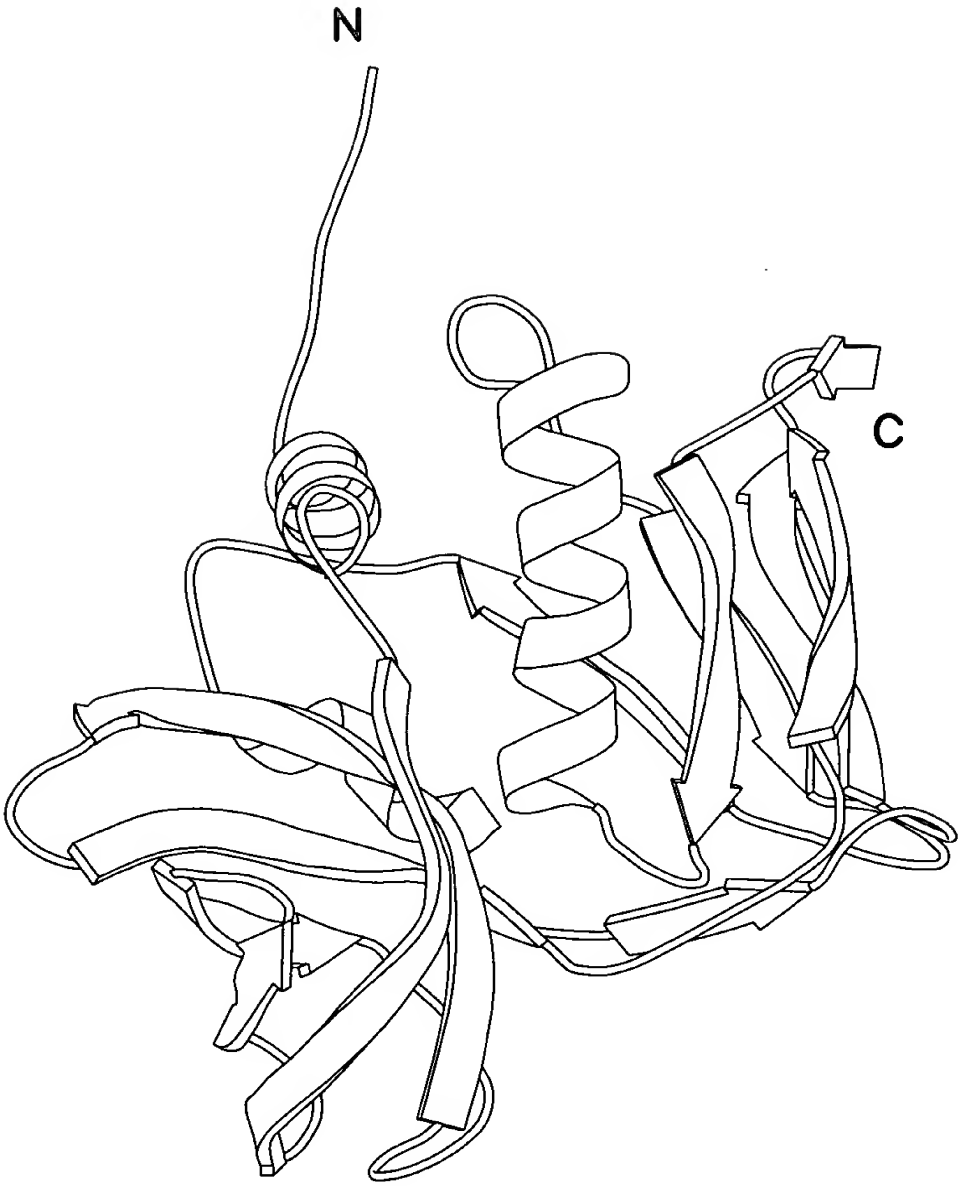
FIG. 2



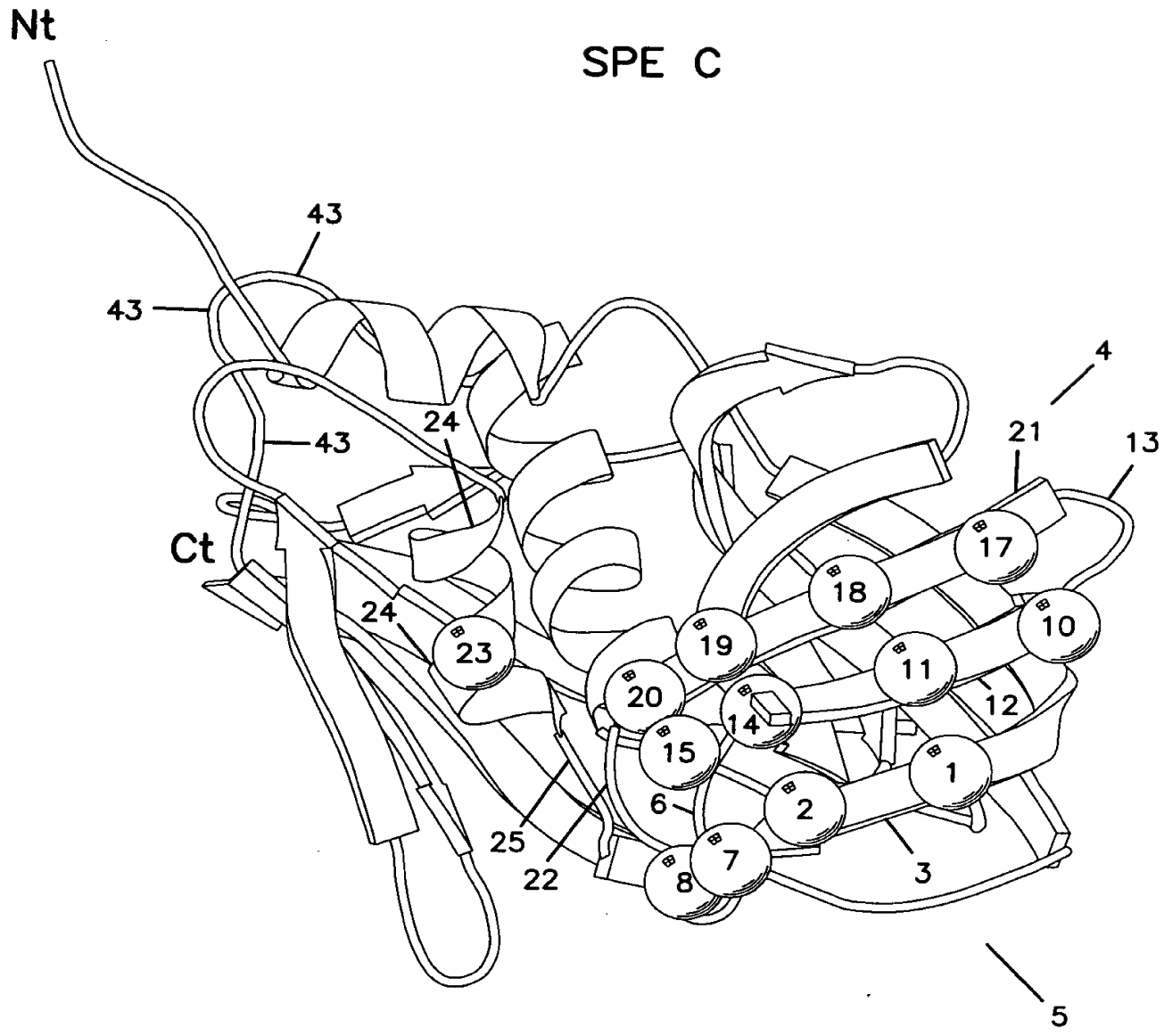
SPE C

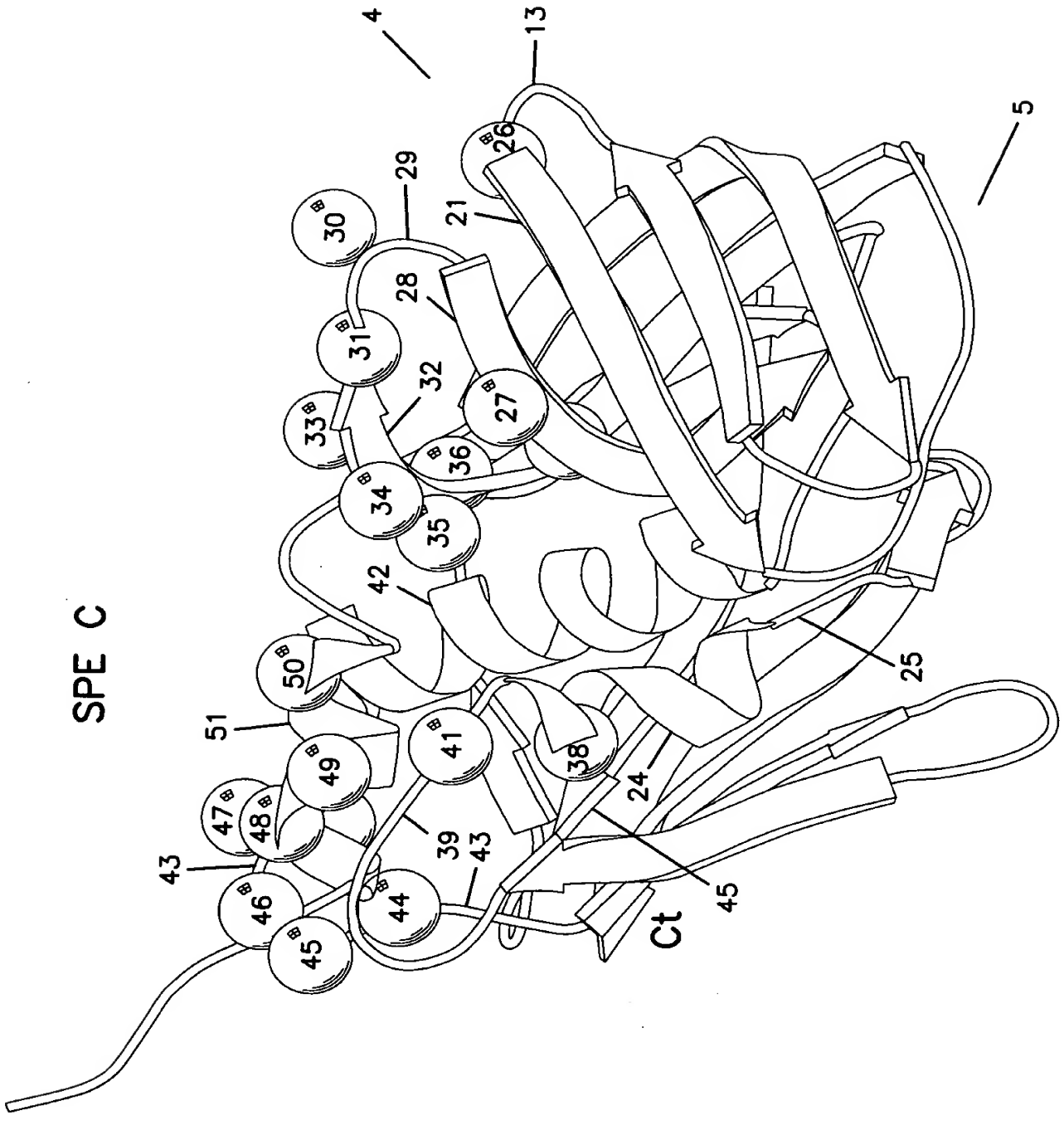
FIG. 3



SPE C

FIG. 4





SPE C

FIG. 5

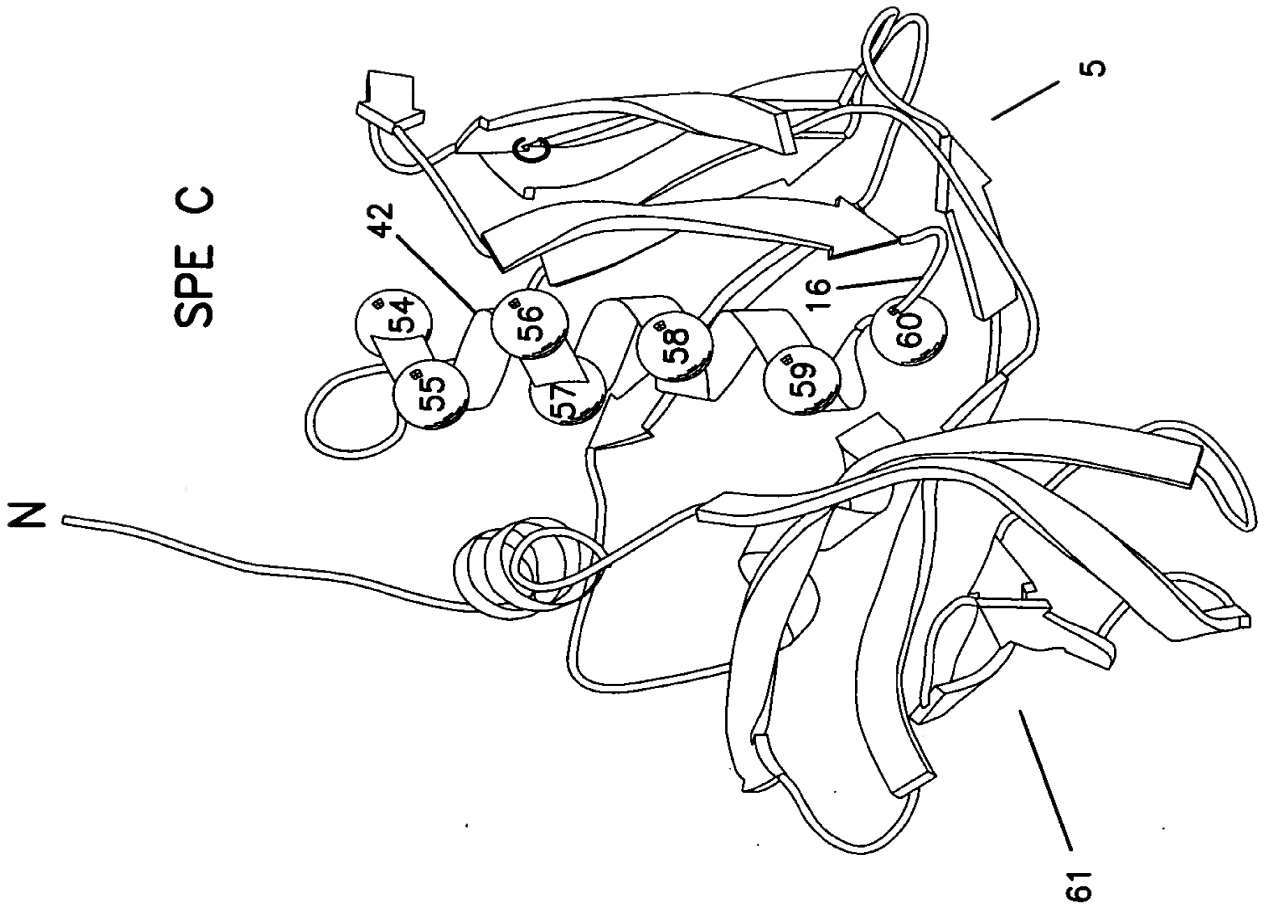


FIG. 6

FIG. 7

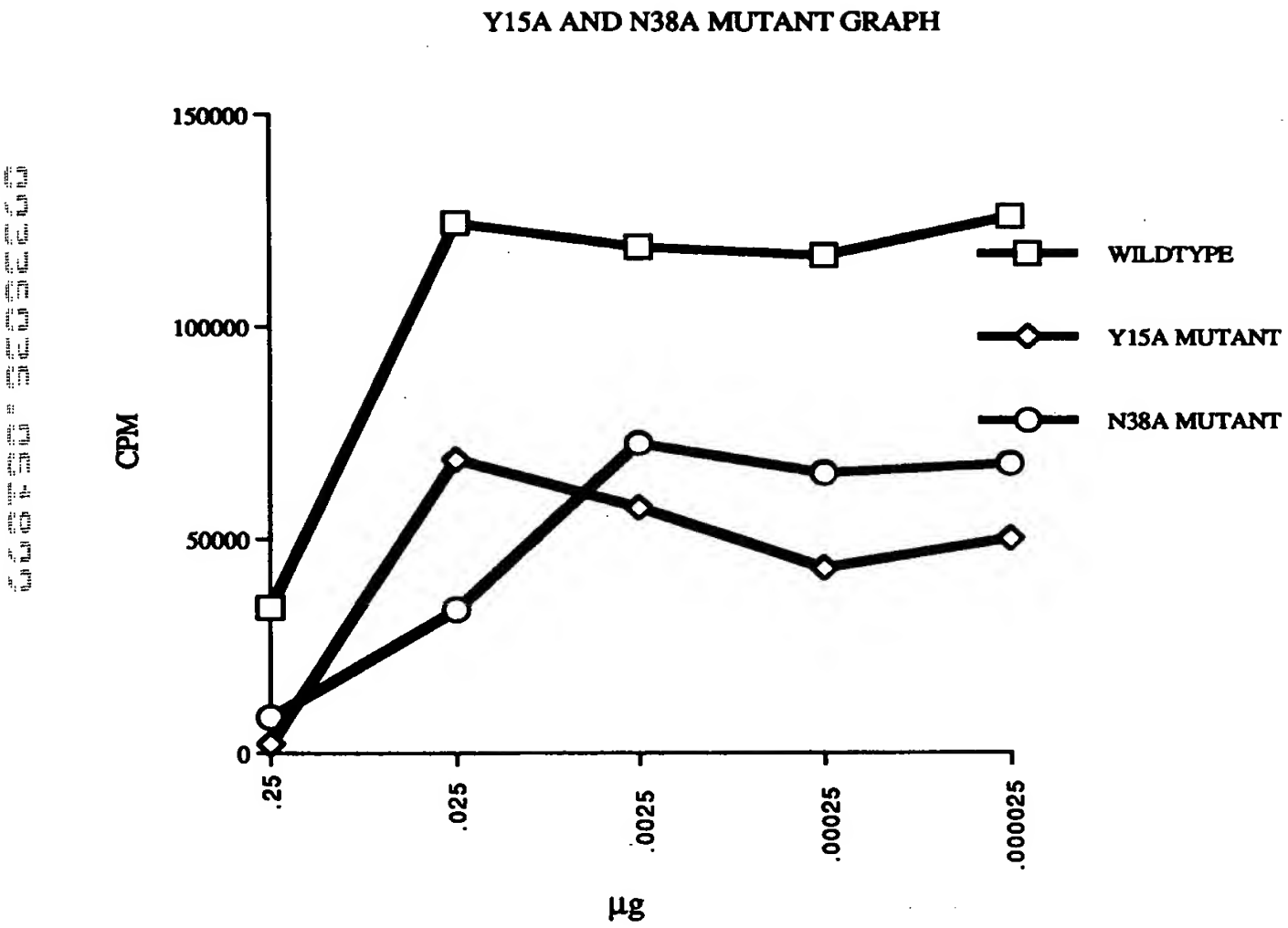


FIG. 8

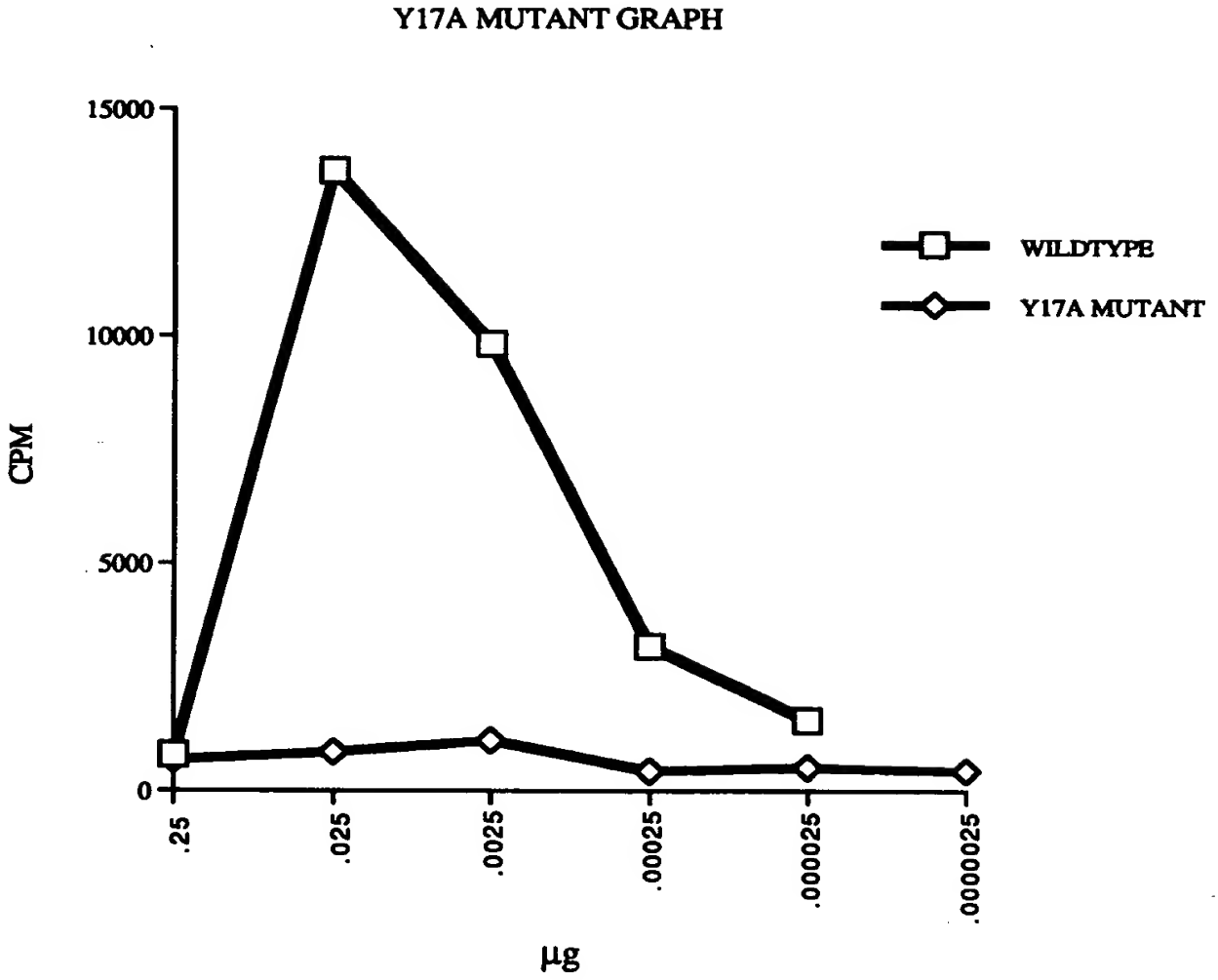


FIG. 9

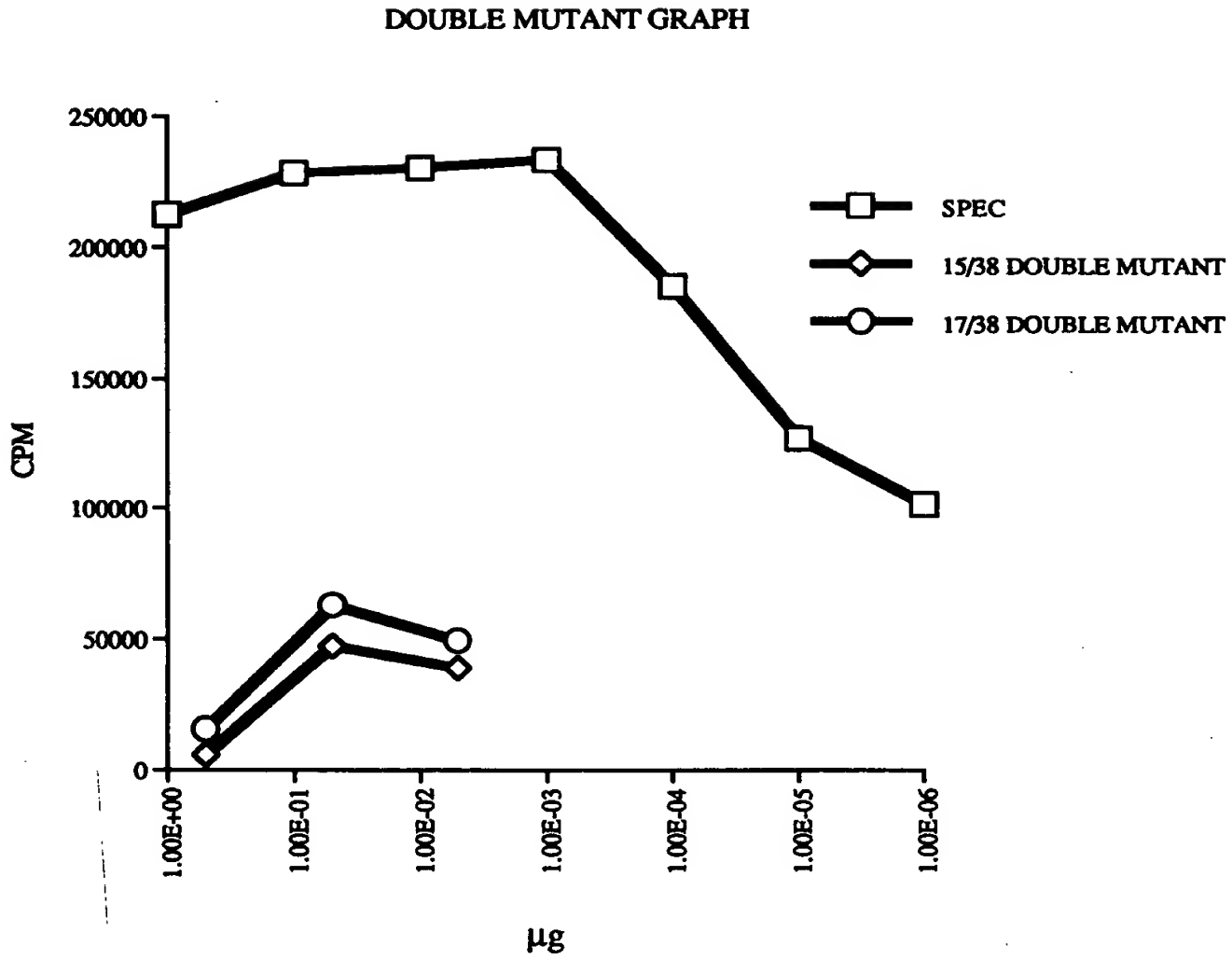
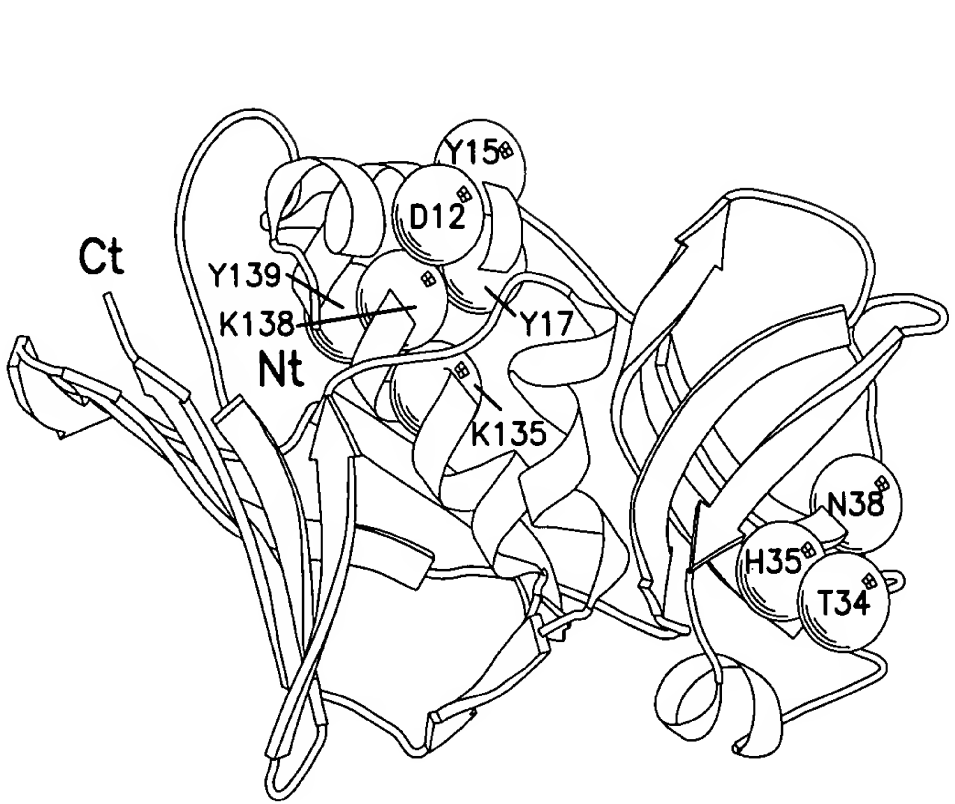
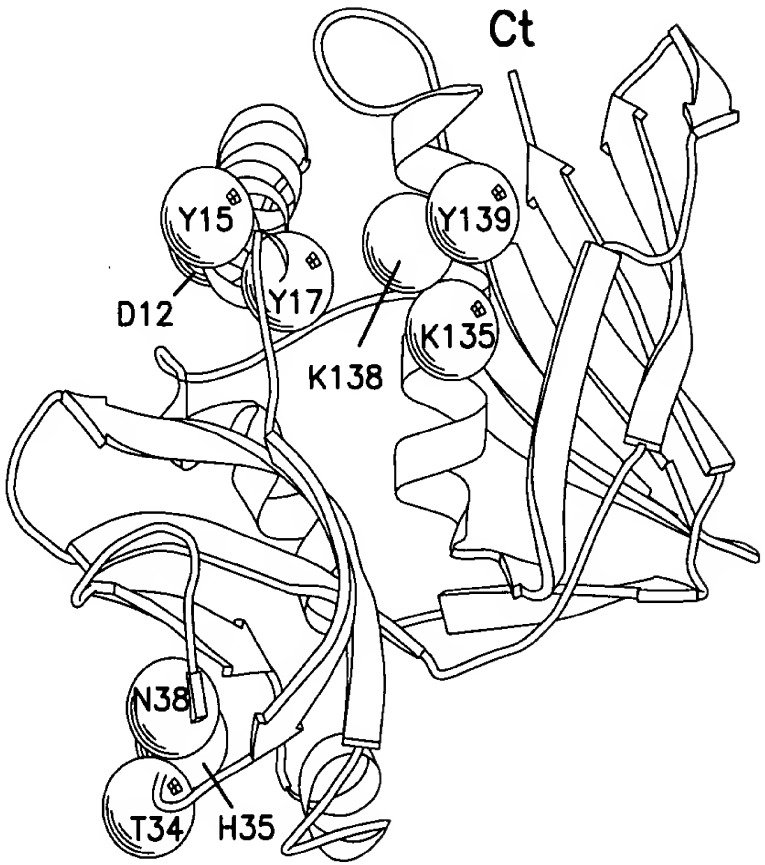


FIG. 10

SPE C



DOMAIN A DOMAIN B



DOMAIN B DOMAIN A